



RECEIVED

SEQUENCE LISTING

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<120> PRODUCTION OF OLIGOSACCHARIDES IN TRANSGENIC PLANTS

<130> ARNO-1-15313

<140> US 09/543,861

<141> 2000-03-24

<150> US 09/019,385

<151> 1998-02-05

<150> US 09/193,385

<151> 1998-11-17

<150> US 08/479,470

<151> 1995-06-07

<150> NL 1000064

<151> 1995-04-05

<150> NL 9401140

<151> 1994-08-07

<160> 12

<170> PatentIn version 3.2

<210> 1

<211> 2094

<212> DNA

<213> Barley

<220>

<221> CDS

<222> (46)..(1923)

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Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
5 10 15 20

gac gac ggt aag cgg acc ggc tgc atg agg tgg tcc ggc tgt gcc acc	153
Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr	
25 30 35	
gtg ctg acg gcc tgg gcc atg ggg gtg gtg gtg gtc ggc gcc acg ctc	201
Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val Gly Ala Thr Leu	
40 45 50	
ctg gcg gga ttg agg atg gag cag gcc gtc gac gag gag ggc ggc ggc	249
Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala	
55 60 65	
ggc ggg ttc ccg tgg agc aac gag atg ctg cag tgg cag cgc agc ggt	297
Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ser Gly	
70 75 80	
tac cat ttc cag acg gcc aag aac tac atg agc gat ccc aac gcc ctg	345
Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu	
85 90 95 100	
atg tat tac cgt gga tgg tac cac atg ttc tac cag tac aac ccg gtg	393
Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val	
105 110 115	
ggc acc gac tgg gac gac ggc atg gag tgg ggc cac gcc gtg tcc cgg	441
Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg	
120 125 130	
aac ctt gtc caa tgg cgc acc ctc cct atc gcc atg gtg gcc gac cag	489
Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met Val Ala Asp Gln	
135 140 145	
tgg tac gac atc ctc gga gtc ctc tgg ggc tcc atg acg gtg cta ccc	537
Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met Thr Val Leu Pro	
150 155 160	
aac ggg acg gtc atc atg atc tac acg ggc gcc acc aac gcc tcc gcc	585
Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr Asn Ala Ser Ala	
165 170 175 180	
gtg gag gtc cag tgc atc gcc acc ccg gcc gac ccc aac gac ccc ctc	633
Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro Asn Asp Pro Leu	
185 190 195	
ctc cgc cgg tgg acc aag cac ccc gcc aac ccc gtc atc tgg tgg ccg	681
Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val Ile Trp Ser Pro	
200 205 210	
ccg ggg gtc ggc acc aag gat ttc cga gac ccg atg acc gcc tgg tac	729
Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met Thr Ala Trp Tyr	
215 220 225	

gac gag tcc gac gag aca tgg cgc acc ctc ctc ggg tcc aag gac gac	777
Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly Ser Lys Asp Asp	
230 235 240	
cac gac ggc cac cac gac ggc atc gcc atg atg tac aag acc aag gac	825
His Asp Gly His His Asp Gly Ile Ala Met Met Tyr Lys Thr Lys Asp	
245 250 255 260	
ttc ctc aac tac gag ctc atc cgc ggc atc ttg cac cgg gtg gtg cgc	873
Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His Arg Val Val Arg	
265 270 275	
acc ggc gag tgg gag tgc atc gac ttc tac ccc gtc ggc cgg aga agc	921
Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg Arg Ser	
280 285 290	
agc gac aac tgc tgc gag atg ctg cac gtg ttg aag ggc agc atg gac	969
Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys Ala Ser Met Asp	
295 300 305	
gac gaa cgg cac gac tac tac tgc ctg ggc acc tac gac tgc ggc gcc	1017
Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr Asp Ser Ala Ala	
310 315 320	
aac acg tgg acg ccc atc gac cgc gag ctc gac ttg ggg atc ggg ctg	1065
Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu Gly Ile Gly Leu	
325 330 335 340	
aga tac gac tgg gga aag ttt tat ggc tcc acc tcc ttc tat gat cgc	1113
Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe Tyr Asp Pro	
345 350 355	
gcc aag aac cgg cgc gtg ctc atg ggg tac gtc ggc gag gtc gac tcc	1161
Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser	
360 365 370	
aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct	1209
Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro	
375 380 385	
agg acg gtg gct ctg gat gag aag acc cgg acg aac ctc ctg ctc tgg	1257
Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp	
390 395 400	
ccc gtt gag gag atc gag acc ctc cgc ctc aat gcc acg gaa ctg acc	1305
Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr	
405 410 415 420	
gac gtt acc att aac act ggc tcc gtc atc cat atc cgc ctc cgc caa	1353
Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln	
425 430 435	

gga act caa ggt cga cat gag gag gcc tct ttc caa ctt gat ggt tcc	1401
Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His Leu Asp Ala Ser	
440 445 450	
gcc gtg ggt gcc ctc aac gag gcc gat gtg ggc tac aac tgc agt agc	1449
Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser	
455 460 465	
agc gcc gcc ggt gtt aac gcc gcc gag cta gcc ccc ttc gcc ctc ctc	1497
Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu	
470 475 480	
gtc ctc gcc gcc ggt gac gcc cgt gcc gag caa acg gcc gtc tac ttc	1545
Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe	
485 490 495 500	
tac gtg tct agg gcc ctt gac gga gcc ctc caa acc agc ttc tgc caa	1593
Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr Ser Phe Cys Gln	
505 510 515	
gat gag ctg aga tog tca cga gcc aag gat gtg acc aag cgt gtc atc	1641
Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr Lys Arg Val Ile	
520 525 530	
ggg agc acg gtg ccg gtg ctc gac ggt gag gct ttg tca atg agg gtg	1689
Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val	
535 540 545	
ctc gtg gat caa tcc atc gtg cag gcc ttc gac atg gcc ggg agg acc	1737
Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr	
550 555 560	
acg atg acc tog ccg gtg tac ccg atg gag tog tat cag gag gca aga	1785
Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg	
565 570 575 580	
gtc tac ttg ttc aac aac gcc acc ggt gcc agc gtg acg gcc gaa agg	1833
Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg	
585 590 595	
ctg gtc gtg caa gag atg gac tog gca caa aac cag ctc tcc aat gag	1881
Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu	
600 605 610	
gac gat gcc atg tat ctt cat caa gtt ctt gaa tct cgt cat	1929
Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His	
615 620 625	
taataagcta cattggatca aagaagatca ccagggaagg gcaattcata cataaatcga	1983
atcattctgc acaacctcgc ttgcagcatg cattgaaaca tctgtatttg gatcatcttc	2043

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2094

<210> 2
 <211> 526
 <212> PRT
 <213> Barley

<400> 2

Met Gly Ser His Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu
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Pro Ser Asp Ala Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser
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Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val
 35 40 45

Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu
 50 55 60

Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp
 65 70 75 80

Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp
 85 90 95

Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln
 100 105 110

Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His
 115 120 125

Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met
 130 135 140

Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met
 145 150 155 160

Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr
 165 170 175

Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro
180 185 190

Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val
195 200 205

Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met
210 215 220

Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly
225 230 235 240

Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr
245 250 255

Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His
260 265 270

Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val
275 280 285

Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys
290 295 300

Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr
305 310 315 320

Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu
325 330 335

Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser
340 345 350

Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly
355 360 365

Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile
370 375 380

Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn
385 390 395 400

Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala
405 410 415

Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile
420 425 430

Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His
435 440 445

Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr
450 455 460

Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro
465 470 475 480

Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Glr Thr
485 490 495

Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr
500 505 510

Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr
515 520 525

Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu
530 535 540

Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met
545 550 555 560

Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr
565 570 575

Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val
580 585 590

Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln
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Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser
610 615 620

Arg His
625

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<220>
<223> Synthetic DNA

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<210> 5
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<220>
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 <213> Barley

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His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu Met
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Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val Gly
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Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg
 35 40 45

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<400> 7

Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg
 1 5 10

<210> 8
 <211> 8
 <212> PFT
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<400> 8

Ser Gly Ser Met Thr Val Leu Pro
 1 5

<210> 9
 <211> 10
 <212> PFT
 <213> Barley

<400> 9

Phe Arg Asp Pro Met Thr Ala Trp Tyr Asp
 1 5 10

<210> 10
 <211> 11

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 <213> Barley

<400> 10

Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe
 1 5 10

<210> 11
 <211> 13
 <212> PRT
 <213> Helianthus tuberosus

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 <222> (6)..(6)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> MISC_FEATURE
 <222> (12)..(13)
 <223> Xaa = unknown

<400> 11

Glu Gln Trp Glu Gly Xaa Phe Met Gln Gln Tyr Xaa Xaa
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<210> 12
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 <212> PRT
 <213> Helianthus tuberosus

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 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Xaa = unknown

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 <222> (7)..(8)
 <223> Xaa = unknown

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 <221> MISC_FEATURE
 <222> (11)..(11)
 <223> Xaa = phenylalanine or leucine

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<221> MISC_FEATURE

<222> (13)..(13)

<223> Xaa = unknown

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